S-40 Towards an integrated understanding of genomic and phenotypic divergence

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Sully

Genomics of sexual isolation and reinforcement in a secondary hybrid zone between two subspecies of the house mouse

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AIMS:

Understanding how reproductive isolation evolves in the context of gene flow is a long-standing riddle of evolutionary biology. Coupling among different barrier traits and loci is expected to be instrumental in generating genome-wide differentiation and strong reproductive isolation. Theory predicts that selection can favour coupling and the further evolution of barrier effects (reinforcement) in the presence of gene flow, but that the genetic architectures of barrier traits will also play a key role. Here, we address the evolution of assortative mating, a key step towards the completion of speciation, and the factors promoting its evolution in a secondary hybrid zone. In the two European subspecies of house mice, Mus musculus musculus and M. m. domesticus, earlier studies have demonstrated olfactory-based assortative mate preference in populations at the edges of their hybrid zone. It has been suggested that this behaviour evolved following the recent secondary contact between the two taxa (~3,000 years ago) in response to selection against hybridisation. By combining transcriptome and whole-genome re-sequencing approaches, we investigate the genomic bases of sexual isolation by assessing expression, sequence and structural divergence among choosy and non-choosy populations. Our results provide new insights on how selection and favorable genomic architectures may have promoted the evolution and reinforcement of sexual isolation in this hybrid zone.